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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: Thomsen *et al.*

Confirmation No. 8725

Application No.: 10/009,945

Art Unit: To Be Assigned

Filed: December 11, 2001

Examiner: To Be Assigned

For: ANTAGONISTS OF BMP AND TGF β
SIGNALING PATHWAYS

Atty Docket No.: 10624-092

TRANSMITTAL OF SEQUENCE LISTING

Assistant Commissioner for Patents
Washington, DC 20231

SIR:

In connection with the above-identified application, and in accordance with 37 C.F.R. § 1.821, Applicant submits herewith a Sequence Listing in paper and computer-readable format pursuant to 37 C.F.R. § 1.821(c) and (e).

I hereby state that the content of the paper and computer-readable copies of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same. I hereby state that the submission herein under 37 C.F.R. § 1.821(g) does not include new matter.

Respectfully submitted,

Date June 21, 2002

Anthony M. Insogna 35,203
Anthony M. Insogna (Reg. No.)

PENNIE & EDMONDS LLP
1155 Avenue of the Americas
New York, New York 10036-2711
(212) 790-9090

Enclosures

by Eileen Z. Fehley 46,097
(Reg. No.)



SEQUENCE LISTING

<110> Thomas Gerald
Wrana, Jeffery

<120> ANTAGONISTS OF BMP AND TGF-BETA SIGNALING PATHWAYS

<130> 10624-092

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<170> PatentIn version 3.1

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 Thr Glu Ala Ser Val Leu Thr Ser Asn Ala Thr Thr Ala Gly Ser Gly
 275 280 285
 Glu Leu Pro Pro Gly Trp Glu Gln Arg Tyr Thr Pro Glu Gly Arg Pro
 290 295 300
 Tyr Phe Val Asp His Asn Thr Arg Thr Thr Trp Val Asp Pro Arg
 305 310 315 320
 Arg Gln Gln Tyr Ile Arg Ser Tyr Gly Gly Pro Asn Asn Ala Thr Ile
 325 330 335
 Gln Gln Gln Pro Val Ser Gln Leu Gly Pro Leu Pro Ser Gly Trp Glu
 340 345 350
 Met Arg Leu Thr Asn Thr Ala Arg Val Tyr Phe Val Asp His Asn Thr
 355 360 365
 Lys Thr Thr Thr Trp Asp Asp Pro Arg Leu Pro Ser Ser Leu Asp Gln
 370 375 380
 Asn Val Pro Gln Tyr Lys Arg Asp Phe Arg Arg Lys Leu Ile Tyr Phe
 385 390 395 400
 Leu Ser Gln Pro Ala Leu His Pro Leu Pro Gly Gln Cys His Ile Lys
 405 410 415
 Val Arg Arg Asn His Ile Phe Glu Asp Ser Tyr Ala Glu Ile Met Arg
 420 425 430
 Gln Ser Ala Thr Asp Leu Lys Lys Arg Leu Met Ile Lys Phe Asp Gly
 435 440 445
 Glu Asp Gly Leu Asp Tyr Gly Gly Leu Ser Arg Glu Tyr Phe Phe Leu
 450 455 460
 Leu Ser His Glu Met Phe Asn Pro Phe Tyr Cys Leu Phe Glu Tyr Ser
 465 470 475 480
 Ser Val Asp Asn Tyr Thr Leu Gln Ile Asn Pro His Ser Gly Ile Asn
 485 490 495
 Pro Glu His Leu Asn Tyr Phe Lys Phe Ile Gly Arg Val Ile Gly Leu
 500 505 510
 Ala Ile Phe His Arg Arg Phe Val Asp Ala Phe Phe Val Val Ser Phe
 515 520 525
 Tyr Lys Met Ile Leu Gln Lys Lys Val Thr Leu Gln Asp Met Glu Ser
 530 535 540
 Met Asp Ala Glu Tyr Tyr Arg Ser Leu Val Trp Ile Leu Asp Asn Asp
 545 550 555 560
 Ile Thr Gly Val Leu Asp Leu Thr Phe Ser Val Glu Asp Asn Cys Phe
 565 570 575

Gly Glu Val Val Thr Ile Asp Leu Lys Pro Asn Gly Arg Asn Ile Glu
 580 585 590
 Val Thr Glu Glu Asn Lys Arg Glu Tyr Val Asp Leu Val Thr Val Trp
 595 600 605
 Ile Gln Lys Arg Ile Glu Glu Gln Phe Asn Ala Phe His Glu Gly Phe
 610 615 620
 Ser Glu Leu Ile Pro Gln Glu Leu Ile Asn Val Phe Asp Glu Arg Glu
 625 630 635 640
 Leu Glu Leu Ile Gly Gly Ile Ser Glu Ile Asp Met Glu Asp Trp
 645 650 655
 Lys Lys His Lys Asp Tyr Arg Ser Tyr Ser Glu Asn Asp Gln Ile Ile
 660 665 670
 Lys Trp Phe Trp Glu Leu Met Asp Glu Trp Ser Asn Glu Lys Lys Ser
 675 680 685
 Arg Leu Leu Gln Phe Thr Thr Gly Thr Ser Arg Ile Pro Val Asn Gly
 690 695 700
 Phe Lys Asp Leu Gln Gly Ser Asp Gly Pro Arg Lys Phe Thr Ile Glu
 705 710 715 720
 Lys Ala Gly Glu Pro Asn Lys Leu Pro Lys Ala His Thr Cys Phe Asn
 725 730 735
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 <212> PRT
 <213> Artificial
 <220>
 <223> Description of Artificial Sequence: Consensus
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 <210> 10
 <211> 11
 <212> PRT
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<223> Description of Artificial Sequence: Consensus

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<223> Description of Artificial Sequence: Consensus

<400> 13
Pro Pro Pro Pro Tyr
1 5
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